

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 10/583,179
Source: FWP
Date Processed by STIC: 6/27/06

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PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
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Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

DATE: 06/27/2006

PATENT APPLICATION: US/10/583,179

TIME: 12:19:05

Input Set : F:\51571-10 Seq 08-05-06 v1.txt

Output Set: N:\CRF4\06272006\J583179.raw

4 <110> APPLICANT: Agency for Science, Technology and Research
 6 <120> TITLE OF INVENTION: Protein Separation Device
 8 <130> FILE REFERENCE: 51571-4
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/583,179
 C--> 10 <141> CURRENT FILING DATE: 2006-06-16
 10 <150> PRIOR APPLICATION NUMBER: US 60/530,608
 11 <151> PRIOR FILING DATE: 2003-12-19
 13 <160> NUMBER OF SEQ ID NOS: 8
 15 <170> SOFTWARE: PatentIn version 3.3
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1647
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Escherichia coli
 23 <220> FEATURE:
 24 <221> NAME/KEY: misc_feature
 25 <223> OTHER INFORMATION: GroEL wildtype DNA sequence
 27 <400> SEQUENCE: 1

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30	gataaatctt	tccgtgcacc	gaccatcacc	aaagatgggt	tttccgttgc	tcgtgaaatc	180
31	gaactggaag	acaagttcga	aaacatgggt	gcgcagatgg	tgaaagaagt	tgcctctaaa	240
32	gcgaacgacg	ctgcaggcga	cggtagccac	actgcaaccg	tactgggtca	ggctatcatc	300
33	actgaaggtc	tgaaagctgt	tgctgcgggc	atgaaccgca	tggaacctga	acgtgggtatc	360
34	gacaaagctg	ttaccgctgc	agttgaagaa	ctgaaagcgc	tgcccgtagc	gtgctctgac	420
35	tctaaagcga	ttgctcaggt	tggtactatc	tccgctaact	ccgacgaaac	cgtaggtaaa	480
36	ctgatcgctg	aagcgaatga	caaagtcggg	aaagaaggcg	ttatcacctg	tgaagacggt	540
37	accgggtctgc	aggacgaact	ggacgtgggt	gaaggtagtc	agttcgaccg	tggtacctg	600
38	tctccttact	tcatacaaaa	gccggaaaact	ggcgtagtag	aactggaaaag	cccgttcatac	660
39	ctgctggctg	acaagaaaat	ctccaacatc	cgcgaaatgc	tgccggttct	ggaagccgtt	720
40	gccaaagcag	gcaaaccgct	gctgatcatc	gctgaagatg	tagaaggcga	agcgctggca	780
41	actctggttg	ttaacacccat	gcgtggcatc	gtgaaagttg	ctgcagttaa	agctccgggc	840
42	ttcggcgatc	gtcgtaaagc	tatgctgcag	gatatcgcaa	ccctgactgg	cggtaccgta	900
43	atctctgaag	agatcggtat	ggagctggaa	aaagcaaccc	tggaagacct	gggtcaggct	960
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46	gaccgtgaaa	aactgcagga	gcgcgtagcg	aaactggcag	gcggcggttg	agttatcaaa	1140
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51	gaaccgtctg	ttgttgctaa	caccgttaaa	ggcggcgacg	gcaactacgg	ttacaacgca	1440
52	gcaaccgaag	aatacggcaa	catgatcgac	atgggtatcc	tggacccaac	caaagtaacc	1500
53	cgttctgctc	tgcatgacgc	ggcttctgtg	gctggcctga	tgatcaccac	cgaatgcatg	1560

pr 3-4
**Does Not Comply
 Corrected Diskette Needed**

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59 <211> LENGTH: 548
61 <212> TYPE: PRT
62 <213> ORGANISM: Escherichia coli
64 <220> FEATURE:
65 <221> NAME/KEY: misc_feature
66 <223> OTHER INFORMATION: GroEL wildtype amino acid sequence
68 <400> SEQUENCE: 2
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70 1 5 10 15
72 Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
73 20 25 30
75 Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
76 35 40 45
78 Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
79 50 55 60
81 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
82 65 70 75 80
84 Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
85 85 90 95
87 Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
88 100 105 110
90 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val
91 115 120 125
93 Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
94 130 135 140
96 Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
97 145 150 155 160
99 Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
100 165 170 175
102 Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
103 180 185 190
105 Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
106 195 200 205
108 Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
109 210 215 220
111 Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val
112 225 230 235 240
114 Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
115 245 250 255
117 Glu Ala Leu Ala Thr Leu Val Val Asn Thr Met Arg Gly Ile Val Lys
118 260 265 270
121 Val Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
122 275 280 285
124 Leu Gln Asp Ile Ala Thr Leu Thr Gly Gly Thr Val Ile Ser Glu Glu
125 290 295 300
127 Ile Gly Met Glu Leu Glu Lys Ala Thr Leu Glu Asp Leu Gly Gln Ala

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128 305          310          315          320
130 Lys Arg Val Val Ile Asn Lys Asp Thr Thr Thr Ile Ile Asp Gly Val
131          325          330          335
133 Gly Glu Glu Ala Ala Ile Gln Gly Arg Val Ala Gln Ile Arg Gln Gln
134          340          345          350
136 Ile Glu Glu Ala Thr Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg
137          355          360          365
139 Val Ala Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala
140          370          375          380
142 Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val Glu Asp Ala Leu
143 385          390          395          400
145 His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val Ala Gly Gly Gly
146          405          410          415
148 Val Ala Leu Ile Arg Val Ala Ser Lys Leu Ala Asp Leu Arg Gly Gln
149          420          425          430
151 Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu Arg Ala Met Glu
152          435          440          445
154 Ala Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val
155          450          455          460
157 Val Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala
158 465          470          475          480
160 Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro
161          485          490          495
163 Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly
164          500          505          510
166 Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp
167          515          520          525
169 Ala Ala Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met
170          530          535          540
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176 <210> SEQ ID NO: 3

177 <211> LENGTH: 1647

178 <212> TYPE: DNA

179 <213> ORGANISM: Escherichia coli

181 <220> FEATURE:

182 <221> NAME/KEY: misc_feature

183 <223> OTHER INFORMATION: GroEL-Asp490Cys DNA sequence

185 <220> FEATURE:

186 <221> NAME/KEY: mutation

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188 <223> OTHER INFORMATION: GAC to TCG

190 <400> SEQUENCE: 3

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192 aacgtactgg cagatgcagt gaaagttacc ctcggtccga aaggccgtaa cgtagttctg 120
193 gataaatctt tcggtgcacc gaccatcacc aaagatgggtg tttccgttgc tcgtgaaatc 180
194 gaactggaag acaagttcga aaacatgggt gcgcagatgg tgaaagaagt tgcctctaaa 240
195 gcgaacgacg ctgcaggcga cggtaccacc actgcaaccg tactggctca ggctatcatc 300
196 actgaaggtc tgaaagctgt tgctgcgggc atgaaccgca tggacctgaa acgtggtatc 360

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see p. 4 TGC is at locations 1468-1470

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199 ctgatcgctg aagcgatgga caaagtcggt aaagaaggcg ttatcacctg tgaagacggt 540
200 accggtctgc aggacgaact ggacgtggtt gaaggtatgc agttcgaccg tggctacctg 600
201 tctccttact tcatcaacaa gccggaaact ggcgtagtag aactggaaag cccgttcctc 660
202 ctgctggctg acaagaaaat ctccaacatc cgcgaaatgc tgccggttct ggaagccgtt 720
203 gccaaagcag gcaaaccgct gctgatcatc gctgaagatg tagaaggcga agcgctggca 780
204 actctggttg ttaacaccat gcgtggcatc gtgaaagttg ctgcagttaa agctccgggc 840
205 ttcggcgatc gtcgtaaagc tatgctgcag gatatcgcaa ccctgactgg cgtaccgta 900
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207 aaacgcgttg tgatcaacaa agacaccacc accatcatcg atggcgtggg cgaagaagct 1020
208 gcaatccagg gccgtgttgc tcagatccgt cagcagattg aagaagcaac ttctgactac 1080
209 gaccgtgaaa aactgcagga gcgcgtagcg aaactggcag gcggcgttgc agttatcaaa 1140
210 gtaggtgctg ctaccgaagt tgaaatgaaa gagaaaaaag cacgcgttga agacgccctg 1200
211 cagcgacccc gtgctgcggt agaagaaggc gtggttgcgt gtggtggtgt tgcgctgac 1260
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213 aaagttgcac tgcgtgcaat ggaagctccg ctgcgtcaga tcgtcctgaa ctgcggcgaa 1380
214 gaaccgtctg ttgttgctaa caccgttaaa ggcgcgacg gcaactacgg ttacaacgca 1440
215 gcaaccgaag aatacggcaa catgatcgcg atgggtatcc tggacccaac caaagtaacc 1500
216 cgttctgctc tgcagtacgc ggcttctgtg gctggcctga tgatcaccac cgaatgcatg 1560
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222 <211> LENGTH: 548

223 <212> TYPE: PRT

224 <213> ORGANISM: Escherichia coli

226 <220> FEATURE:

227 <221> NAME/KEY: misc_feature

228 <223> OTHER INFORMATION: GroEL Asp490Cys amino acid sequence

230 <220> FEATURE:

231 <221> NAME/KEY: SITE

232 <222> LOCATION: (490)..(490)

233 <223> OTHER INFORMATION: D to C

235 <400> SEQUENCE: 4

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239 Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
240 20 25 30
241 Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
242 35 40 45
244 Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
245 50 55 60
247 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
248 65 70 75 80
250 Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
251 85 90 95
253 Gln Ala Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
254 100 105 110
256 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Thr Ala Ala Val

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263	145					150					155					160
265	Leu	Ile	Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr
266					165					170						175
268	Val	Glu	Asp	Gly	Thr	Gly	Leu	Gln	Asp	Glu	Leu	Asp	Val	Val	Glu	Gly
269				180					185					190		
271	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Lys	Pro
272			195					200					205			
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275		210					215					220				
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278	225				230						235					240
280	Ala	Lys	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly
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284			260					265						270		
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287		275					280					285				
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290		290				295					300					
292	Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Gln	Ala
293	305				310						315				320	
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296				325					330					335		
298	Gly	Glu	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Ala	Gln	Ile	Arg	Gln	Gln
299			340					345					350			
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302		355					360						365			
304	Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala
305		370				375					380					
307	Thr	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Ala	Arg	Val	Glu	Asp	Ala	Leu
308	385				390						395					400
310	His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	Ala	Gly	Gly	Gly
311				405					410					415		
313	Val	Ala	Leu	Ile	Arg	Val	Ala	Ser	Lys	Leu	Ala	Asp	Leu	Arg	Gly	Gln
314			420					425					430			
316	Asn	Glu	Asp	Gln	Asn	Val	Gly	Ile	Lys	Val	Ala	Leu	Arg	Ala	Met	Glu
317		435					440						445			
319	Ala	Pro	Leu	Arg	Gln	Ile	Val	Leu	Asn	Cys	Gly	Glu	Glu	Pro	Ser	Val
320		450				455					460					
322	Val	Ala	Asn	Thr	Val	Lys	Gly	Gly	Asp	Gly	Asn	Tyr	Gly	Tyr	Asn	Ala
323	465				470						475					480
325	Ala	Thr	Glu	Glu	Tyr	Gly	Asn	Met	Ile	Cys	Met	Gly	Ile	Leu	Asp	Pro
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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date